

SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Ligand binding domains of Ultraspiracle (USP) proteins

<130> Le A 34 772

<140>

<141>

<150> DE 100 36 461.6

<151> 2000-07-25

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 262

<212> PRT

<213> *Heliothis virescens*

<400> 1

Val Gln Glu Leu Ser Ile Glu Arg Leu Leu Glu Met Glu Ser Leu Val
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Ala Asp Pro Ser Glu Glu Phe Gln Phe Leu Arg Val Gly Pro Asp Ser
20 25 30

Asn Val Pro Pro Lys Phe Arg Ala Pro Val Ser Ser Leu Cys Gln Ile
35 40 45

Gly Asn Lys Gln Ile Ala Ala Leu Val Val Trp Ala Arg Asp Ile Pro
50 55 60

His Phe Ser Gln Leu Glu Met Glu Asp Gln Ile Leu Leu Ile Lys Gly
65 70 75 80

Ser Trp Asn Glu Leu Leu Leu Phe Ala Ile Ala Trp Arg Ser Met Glu
85 90 95

Phe Leu Thr Glu Glu Arg Asp Gly Val Asp Gly Thr Gly Asn Arg Thr
100 105 110

Thr Ser Pro Pro Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu His
115 120 125

Arg Asn Ser Ala Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val
130 135 140

Leu Ser Glu Leu Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala
145 150 155 160

Glu Tyr Val Ala Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys
165 170 175

Gly Leu Lys Asn Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe
180 185 190

Leu Cys Leu Asp Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly
195 200 205

Arg Phe Ala Ala Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser
210 215 220

Leu Lys Ser Phe Glu His Leu Phe Phe Phe His Leu Val Ala Asp Thr
225 230 235 240

Ser Ile Ala Gly Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro
245 250 255

Ile Asp Thr Asn Met Met
260

<210> 2

<211> 466

<212> PRT

<213> *Heliothis virescens*

<400> 2

Met Ser Val Ala Lys Lys Asp Lys Pro Thr Met Ser Val Thr Ala Leu
1 5 10 15

Ile Asn Trp Ala Arg Pro Leu Pro Pro Gly Gln Gln Gln Gln Pro Met
20 25 30

Thr Pro Thr Ser Pro Gly Asn Met Leu Gln Pro Met Ala Thr Pro Ser
35 40 45

Asn Leu Pro Thr Val Asp Cys Ser Leu Asp Ile Gln Trp Leu Asn Leu
50 55 60

Glu Gly Gly Phe Met Ser Pro Met Ser Pro Pro Glu Met Lys Pro Asp

0000556.072001

65		70		75		80
Thr Ala Met Leu Asp Gly Leu Arg Asp Asp Ser Thr Pro Pro Pro Ala						
	85			90		95
Phe Lys Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu						
	100		105			110
Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr						
	115		120			125
Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp						
	130		135			140
Leu Thr Tyr Ala Cys Arg Glu Glu Arg Asn Cys Ile Ile Asp Lys Arg						
	145		150		155	160
Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Cys						
	165		170			175
Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Ala Ala Arg						
	180		185			190
Gly Thr Glu Asp Ala His Pro Ser Ser Ser Val Gln Val Gln Glu Leu						
	195		200			205
Ser Ile Glu Arg Leu Leu Glu Met Glu Ser Leu Val Ala Asp Pro Ser						
	210		215			220
Glu Glu Phe Gln Phe Leu Arg Val Gly Pro Asp Ser Asn Val Pro Pro						
	225		230		235	240
Lys Phe Arg Ala Pro Val Ser Ser Leu Cys Gln Ile Gly Asn Lys Gln						
	245		250			255
Ile Ala Ala Leu Val Val Trp Ala Arg Asp Ile Pro His Phe Ser Gln						
	260		265			270
Leu Glu Met Glu Asp Gln Ile Leu Leu Ile Lys Gly Ser Trp Asn Glu						
	275		280			285
Leu Leu Leu Phe Ala Ile Ala Trp Arg Ser Met Glu Phe Leu Thr Glu						
	290		295			300
Glu Arg Asp Gly Val Asp Gly Thr Gly Asn Arg Thr Thr Ser Pro Pro						
	305		310		315	320
Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu His Arg Asn Ser Ala						

325

330

335

Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val Leu Ser Glu Leu
340 345 350

Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala Glu Tyr Val Ala
355 360 365

Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys Gly Leu Lys Asn
370 375 380

Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe Leu Cys Leu Asp
385 390 395 400

Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly Arg Phe Ala Ala
405 410 415

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser Leu Lys Ser Phe
420 425 430

Glu His Leu Phe Phe Phe His Leu Val Ala Asp Thr Ser Ile Ala Gly
435 440 445

Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro Ile Asp Thr Asn
450 455 460

Met Met
465

4